

FIG. 1

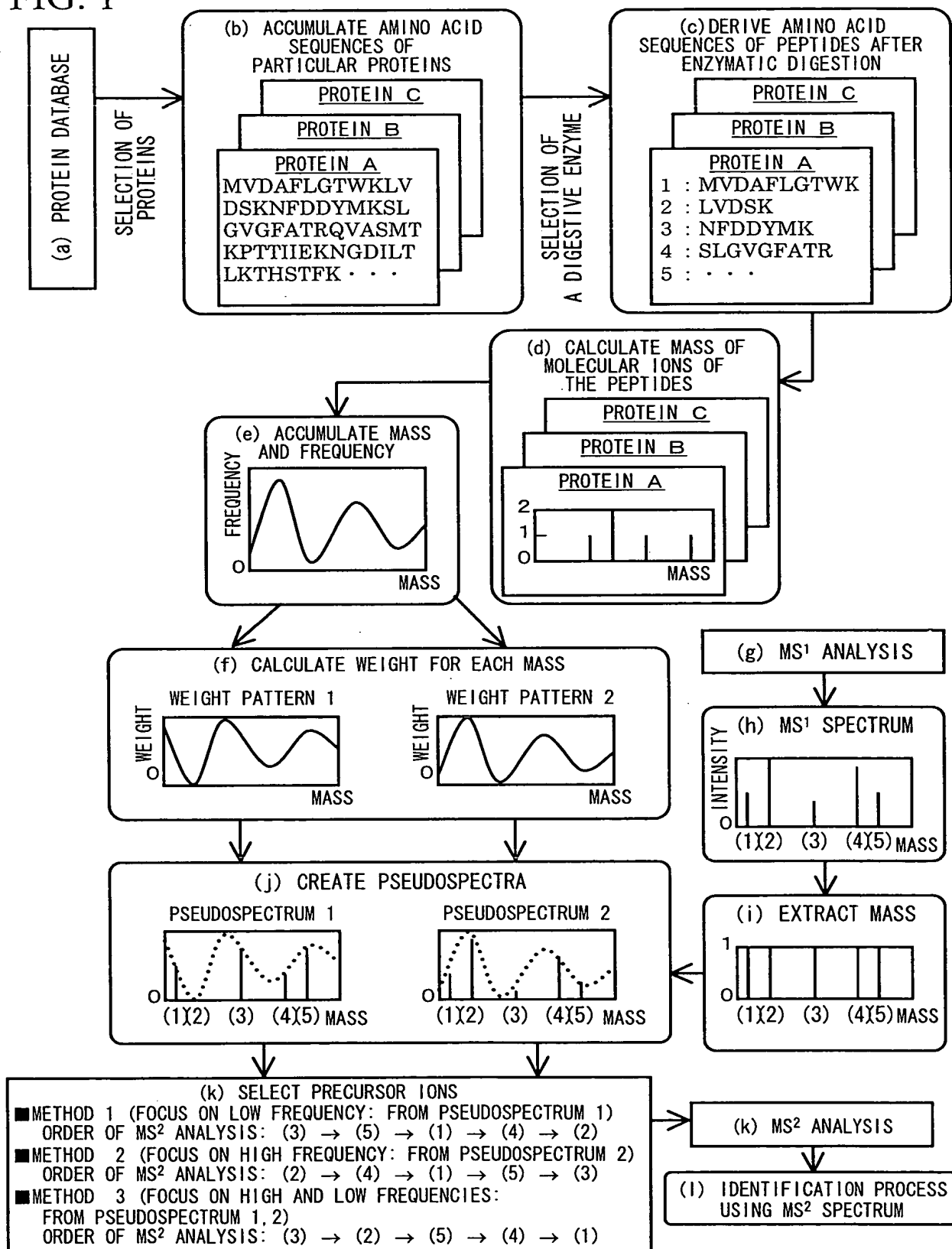


FIG. 2

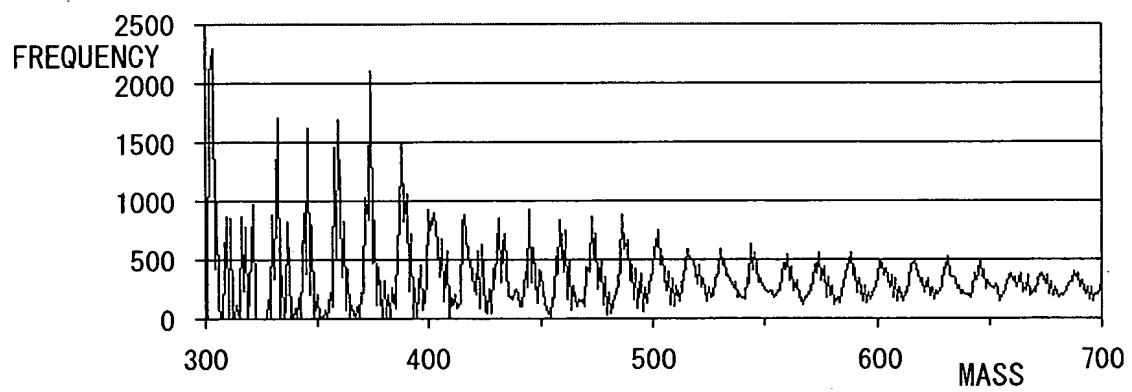
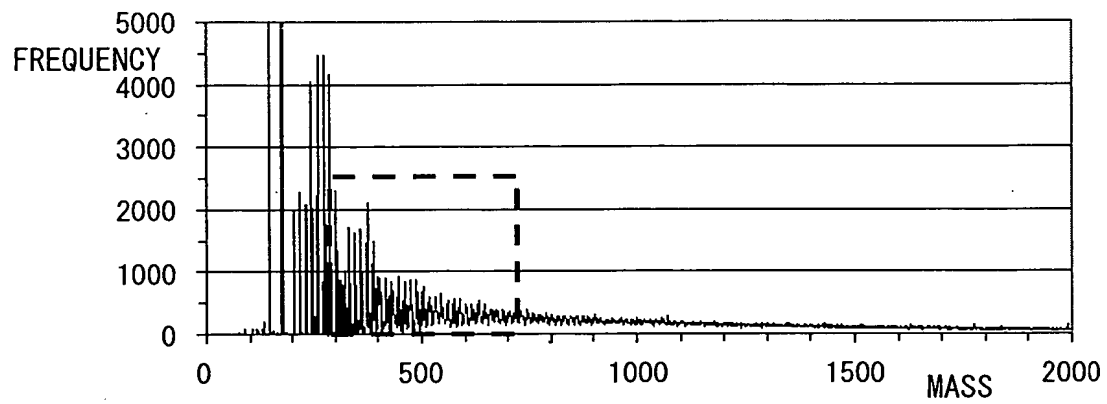


FIG. 3

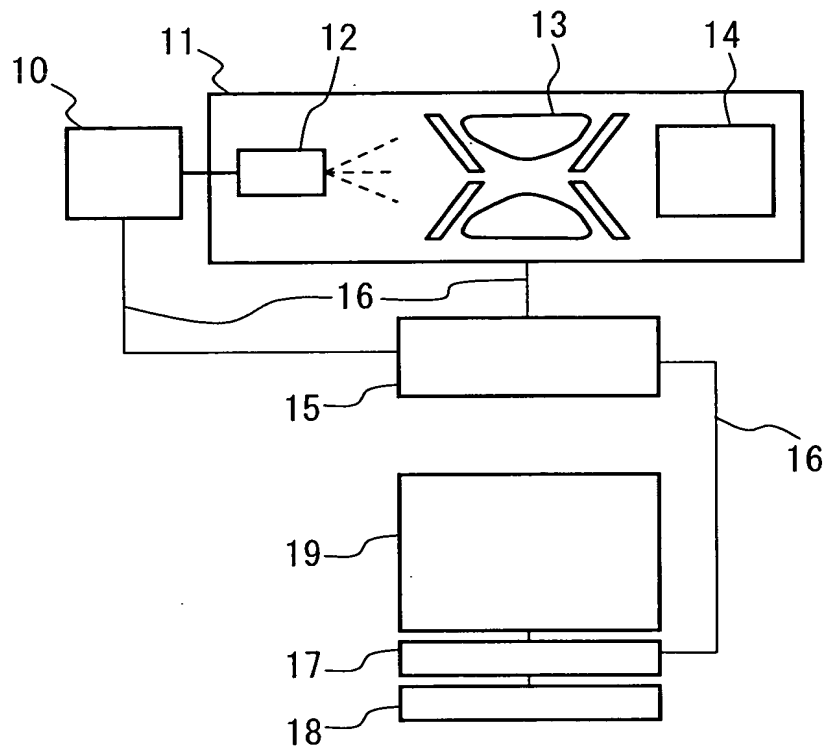


FIG. 4

(a) PROTEIN SELECTION CONDITIONS

DATABASE Swiss-prot ▼ SPECIES homo sapiens ▼

KEYWORD zinc finger

(b) FREQUENCY AND WEIGHT PATTERN CALCULATION CONDITIONS

MODIFICATION ☐ PHOSPHORIZATION ☐ ACETYLATION ☐ METHYLATION

DIGESTIVE ENZYME Trypsin ▼

METHOD OF IONIZATION ESI ▼

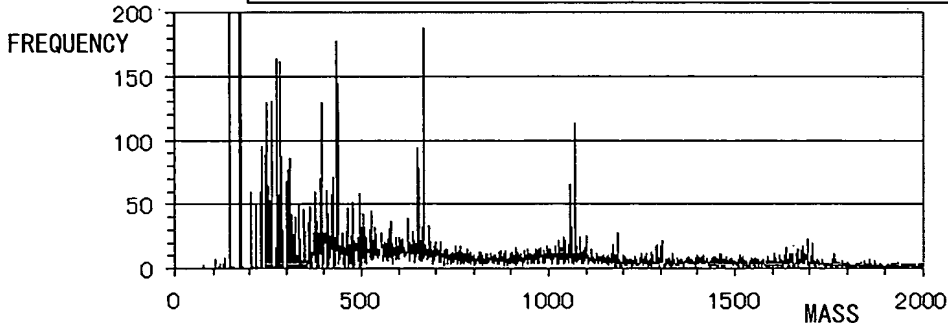
MASS ACCURACY (Da) 1

MASS RANGE (Da) 50 – 40000

MASS TYPE ☒ MONOISOTOPIC ☐ AVERAGE

(c) FREQUENCY AND WEIGHT PATTERN CALCULATION RESULTS

☒ FREQUENCY ☐ WEIGHT PATTERN 1 ☐ WEIGHT PATTERN 2



(d) PRECURSOR ION SELECTION AND MS/MS ANALYSIS CONDITIONS

MASS RANGE (Da) 300 – 40000

THRESHOLD OF ION INTENSITY 10 % ▼

PSEUDOSPECTRUM INTENSITY (LOW FREQUENCY) 0.5 – 0.001

PSEUDOSPECTRUM INTENSITY (HIGH FREQUENCY) 1 – 0.01

PRECURSOR ION ☒ FROM LOW FREQUENCY ☐ FROM HIGH FREQUENCY  
☐ HIGH → LOW ALTERNATELY ☐ LOW → HIGH ALTERNATELY

MS/MS ANALYSIS REPETITION 3 TIMES ▼

FIG. 5

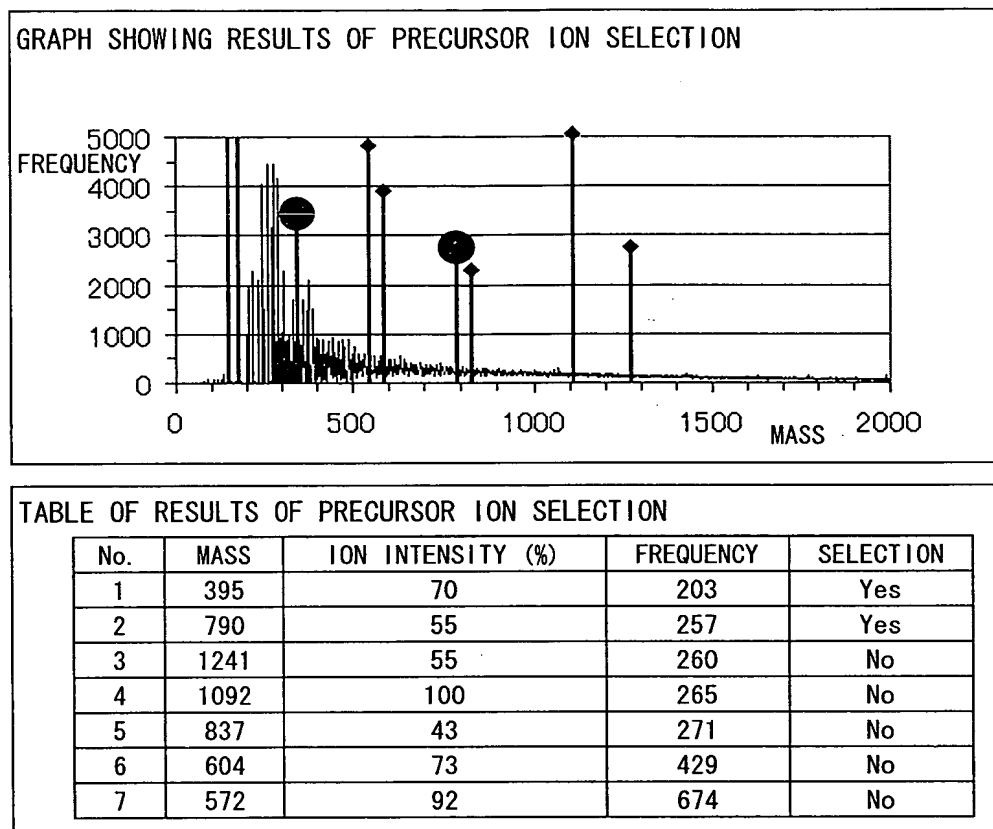


FIG. 6

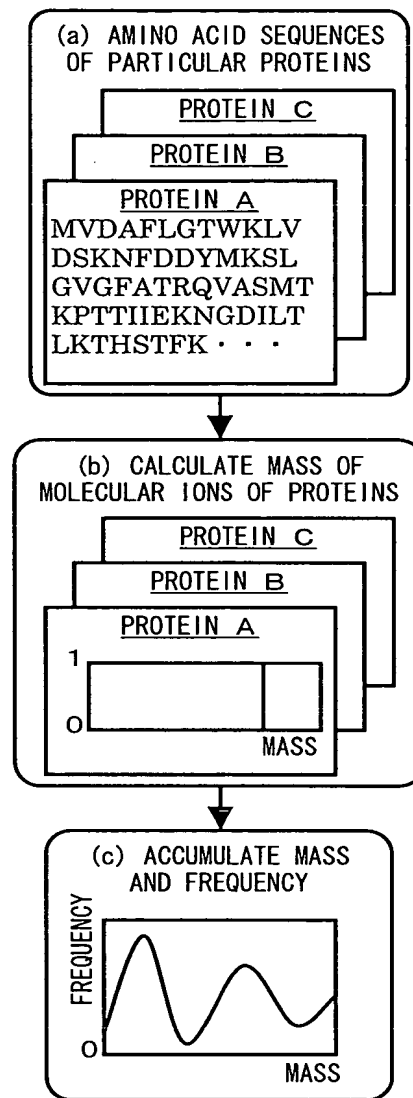


FIG. 7

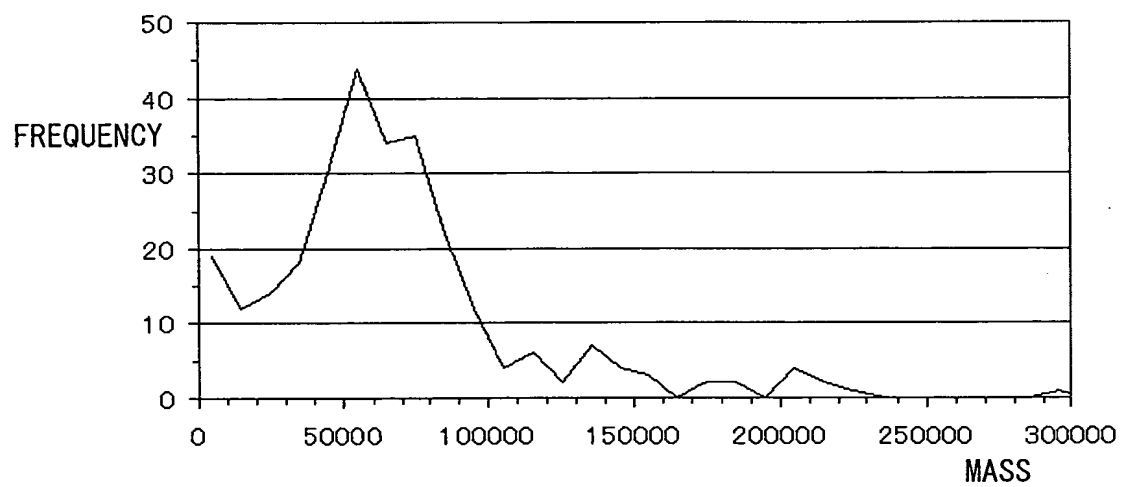


FIG. 8

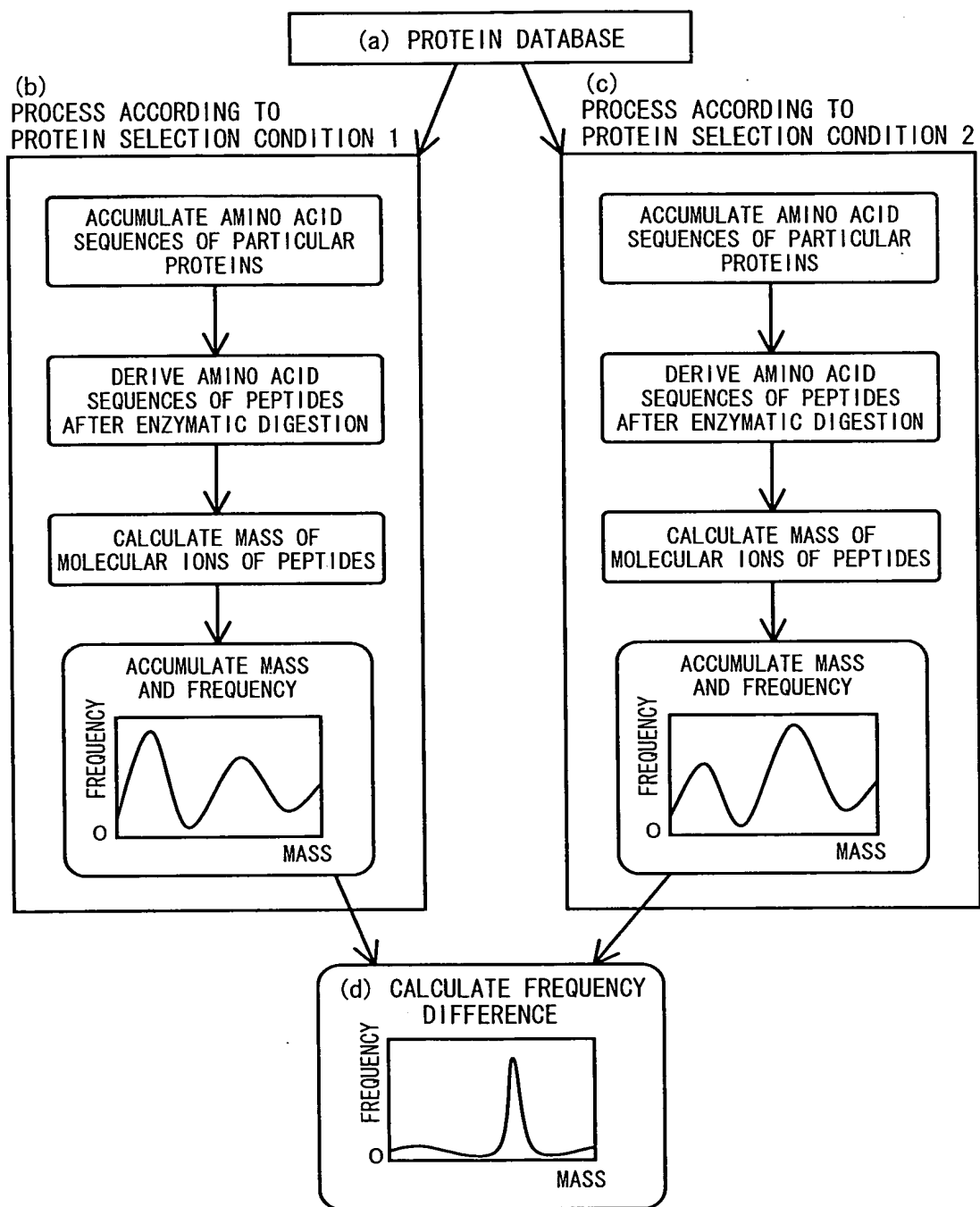




FIG. 9

